

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

CHUGAI SEIYAKU KABUSHIKI KAISHA

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<170> PatentIn Ver. 2.0

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Val Ala Asp Pro Glu Pro Leu Gly Leu Phe Ser Glu Gly Glu Leu Met

5

10

15

tcg gtg ggc atg gac acc ttc atc cac cgc atc gac tcc acc gag gta 152

Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr Glu Val

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atc tac cag ccg cgc cgc aaa cgc gcc aag ctc atc ggc aag tac ctg 200

Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys Tyr Leu

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atg ggg gac ctg ctc ggg gag ggc tcg tac ggc aag gtg aag gag gtg 248

Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys Glu Val

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ctg gac tcc gag acc tta tgc cgc agg gcg gtc aag atc ctc aag aag 296

Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu Lys Lys

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aaa aag ctg cgc agg atc ccc aat gga gag gcc aac gtc aag aag gag 344

Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys Lys Glu

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atc cag ctg ctg cgg cgg ctg cgg cat cgg aat gtg atc cag ctt gtg 392

Ile Gln Leu Leu Arg Arg Leu Arg His Arg Asn Val Ile Gln Leu Val

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gac gtg ctg tac aat gag gag aag cag aag atg tat atg gtg atg gag 440

Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val Met Glu

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tac tgc gta tgt ggc atg cag gag atg ctg gac agt gtg ccg gag aag 488

Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro Glu Lys

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cgc ttc cct gtg tgc caa gct cat ggg tac ttc cgc cag ctg att gac 536

Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Arg Gln Leu Ile Asp

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ggc ctg gaa tac cta cac agc cag ggc att gtt cac aag gac atc aag 584

Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp Ile Lys

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ccg ggc aac ctg cta ctc acc acc aat ggc aca ctc aag atc tcc gac 632
 Pro Gly Asn Leu Leu Leu Thr Thr Asn Gly Thr Leu Lys Ile Ser Asp
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 Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Val Asp Asp Thr Cys
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cgg aca agc cag ggc tcc ccg gcc ttc cag cct cct gag att gcc aat 728
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 Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser Ala Gly
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aat atc tac aag ctc ttt gag aac att ggg aga gga gac ttc acc atc 872
 Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Arg Gly Asp Phe Thr Ile
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 Pro Cys Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Arg Gly Met Leu

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Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg Gln His				
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agc tgg ttc cgg aag aaa cac cct ctg gct gag gcg ctc gta cct atc				1016
Ser Trp Phe Arg Lys Lys His Pro Leu Ala Glu Ala Leu Val Pro Ile				
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cca cca agc cca gac act aag gac cgc tgg cgc agt atg act gta gtg				1064
Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr Val Val				
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ccc tac ctg gag gac ctg cat ggc cgt gcg gag gag gag gag gag gaa				1112
Pro Tyr Leu Glu Asp Leu His Gly Arg Ala Glu Glu Glu Glu Glu Glu				
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gac ttg ttt gac att gag gac ggc att atc tac acc cag gac ttc aca				1160
Asp Leu Phe Asp Ile Glu Asp Gly Ile Ile Tyr Thr Gln Asp Phe Thr				
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Val Pro Gly Gln Val Leu Glu Glu Glu Val Gly Gln Asn Gly Gln Ser				
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His Ser Leu Pro Lys Ala Val Cys Val Asn Gly Thr Glu Pro Gln Leu

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Ser Ser Lys Val Lys Pro Glu Gly Arg Pro Gly Thr Ala Asn Pro Ala

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Arg Lys Val Cys Ser Ser Asn Lys Ile Arg Arg Leu Ser Ala Cys Lys

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Gln Gln

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Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr

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Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys

35 40 45

Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys

50 55 60

Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu

65 70 75 80

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys

85

90

95

Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Arg Asn Val Ile Gln

100

105

110

Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val

115

120

125

Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro

130

135

140

Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Arg Gln Leu

145

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155

160

Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp

165

170

175

Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Asn Gly Thr Leu Lys Ile

180

185

190

Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Val Asp Asp

195

200

205

Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile

210

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Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
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Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
 245 250 255

Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Arg Gly Asp Phe
 260 265 270

Thr Ile Pro Cys Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Arg Gly
 275 280 285

Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
 290 295 300

Gln His Ser Trp Phe Arg Lys Lys His Pro Leu Ala Glu Ala Leu Val
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Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
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Val Val Pro Tyr Leu Glu Asp Leu His Gly Arg Ala Glu Glu Glu Glu
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Glu Glu Asp Leu Phe Asp Ile Glu Asp Gly Ile Ile Tyr Thr Gln Asp

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365

Phe Thr Val Pro Gly Gln Val Leu Glu Glu Glu Val Gly Gln Asn Gly

370

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Gln Ser His Ser Leu Pro Lys Ala Val Cys Val Asn Gly Thr Glu Pro

385

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395

400

Gln Leu Ser Ser Lys Val Lys Pro Glu Gly Arg Pro Gly Thr Ala Asn

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Pro Ala Arg Lys Val Cys Ser Ser Asn Lys Ile Arg Arg Leu Ser Ala

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Cys Lys Gln Gln

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<213> Artificial Sequence

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<400> 14

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aattcgataa cttcgtataa tgtatgctat acgaagttat gaagcttga 109

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 15

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36

<210> 16

<211> 86

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 16

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86

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 17

ccggtgttcc acataacttc

20

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 18

gtttcccaag ctttatttat tgcc

24

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 19

cagcagcaag gtgaagccag aagg

24

<210> 20

<211> 24

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

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24

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

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<210> 22

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<212> DNA

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 22

ctctcccaaa ccctctgact

20